Iris Flower Clustering

Using K-Means Machine Learning Algorithms

This project demonstrates how machine learning algorithms can be used to clustering for iris.

```
In [42]: import pandas as pd
         import numpy as np
         import seaborn as sns
         import matplotlib.pyplot as plt
         from sklearn.cluster import KMeans
         from sklearn.metrics import silhouette_score
```

```
In [43]: df = pd.read_csv("F:\\Machine Learning\\Iris flower dataset\\IRIS.csv")
```

```
In [44]: df.head()
```

Out[44]:

	sepal_length	sepal_width	petal_length	petal_width	species
0	5.1	3.5	1.4	0.2	Iris-setosa
1	4.9	3.0	1.4	0.2	Iris-setosa
2	4.7	3.2	1.3	0.2	Iris-setosa
3	4.6	3.1	1.5	0.2	Iris-setosa
4	5.0	3.6	1.4	0.2	Iris-setosa

In [45]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 150 entries, 0 to 149
Data columns (total 5 columns):
 #   Column        Non-Null Count  Dtype  
---  ------        --------------  -----  
 0   sepal_length  150 non-null    float64
 1   sepal_width   150 non-null    float64
 2   petal_length  150 non-null    float64
 3   petal_width   150 non-null    float64
 4   species       150 non-null    object 
dtypes: float64(4), object(1)
memory usage: 6.0+ KB
```

In [46]:
```
df.describe()
```

Out[46]:

	sepal_length	sepal_width	petal_length	petal_width
count	150.000000	150.000000	150.000000	150.000000
mean	5.843333	3.054000	3.758667	1.198667
std	0.828066	0.433594	1.764420	0.763161
min	4.300000	2.000000	1.000000	0.100000
25%	5.100000	2.800000	1.600000	0.300000
50%	5.800000	3.000000	4.350000	1.300000
75%	6.400000	3.300000	5.100000	1.800000
max	7.900000	4.400000	6.900000	2.500000

In [47]:
```
df['species'].unique()
```

Out[47]:
```
array(['Iris-setosa', 'Iris-versicolor', 'Iris-virginica'], dtype=object)
```

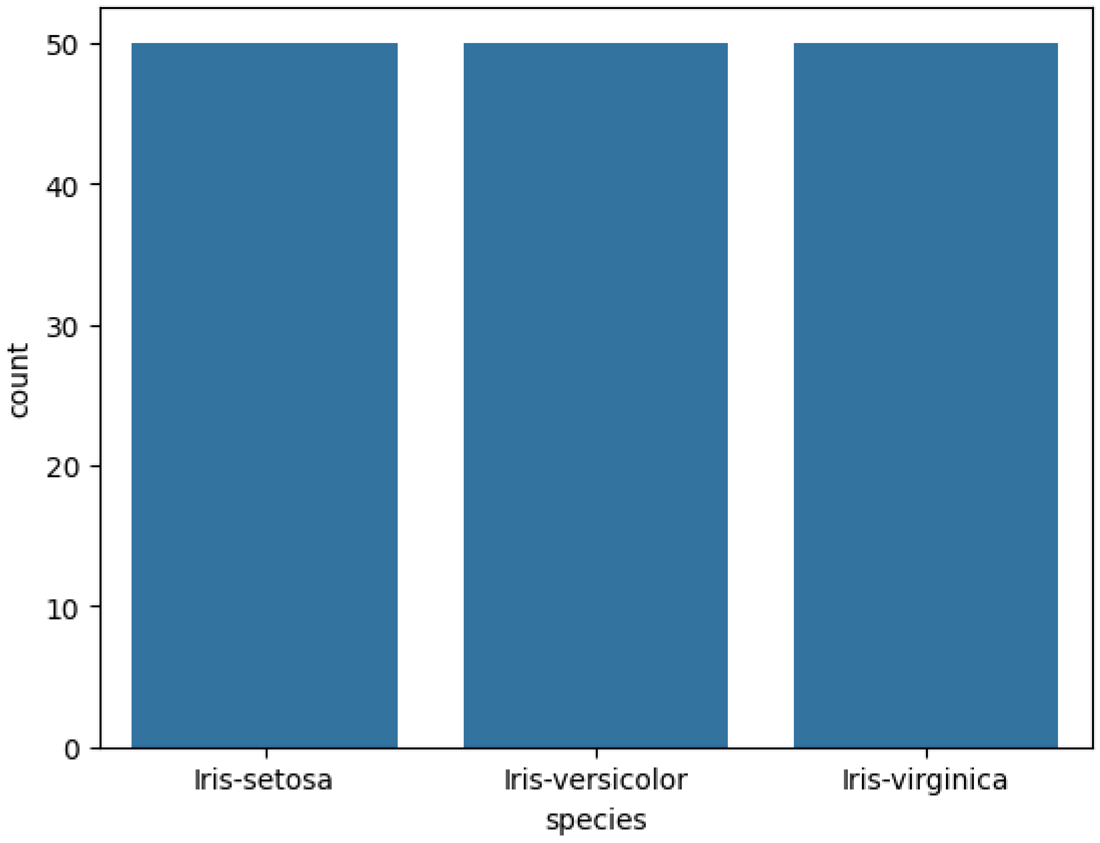
In [48]:
```
pd.crosstab(index=df["species"], columns="count")
```

Out[48]:

col_0	count
species	
Iris-setosa	50
Iris-versicolor	50
Iris-virginica	50

In [49]:
```
sns.countplot(data= df , x = 'species')
```

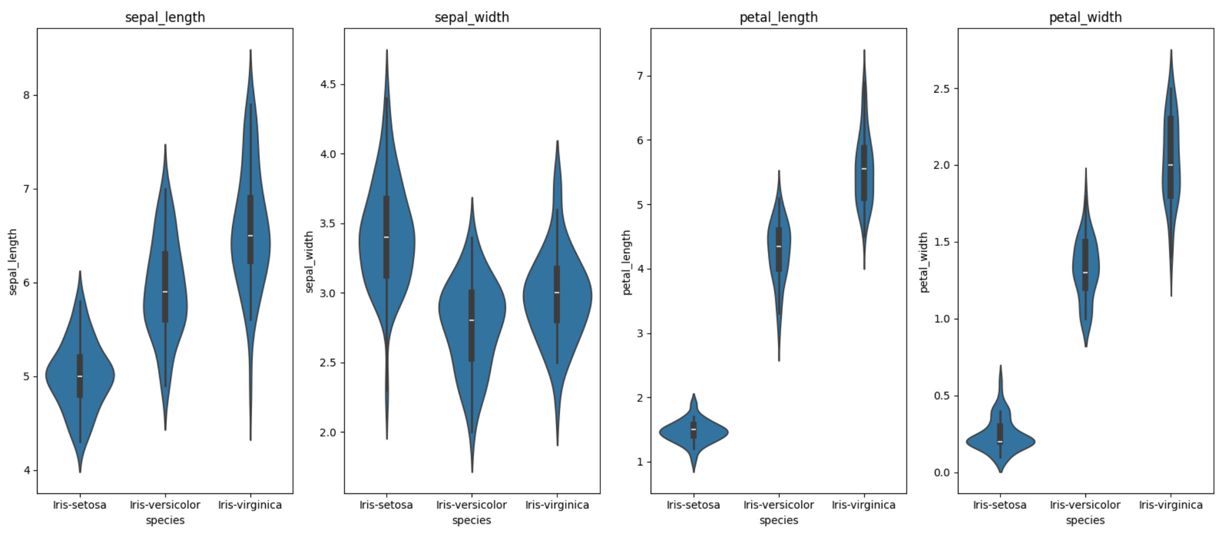
Out[49]:
```
<Axes: xlabel='species', ylabel='count'>
```



In [50]:
```
features = ['sepal_length','sepal_width','petal_length','petal_width']
fig, axes = plt.subplots(1, len(features), figsize=(16, 7))

for i , feature in enumerate(features) :
    sns.violinplot(x="species", y=feature, data=df , ax= axes[i])
    axes[i].set_title(feature)

plt.tight_layout()
plt.show()
```



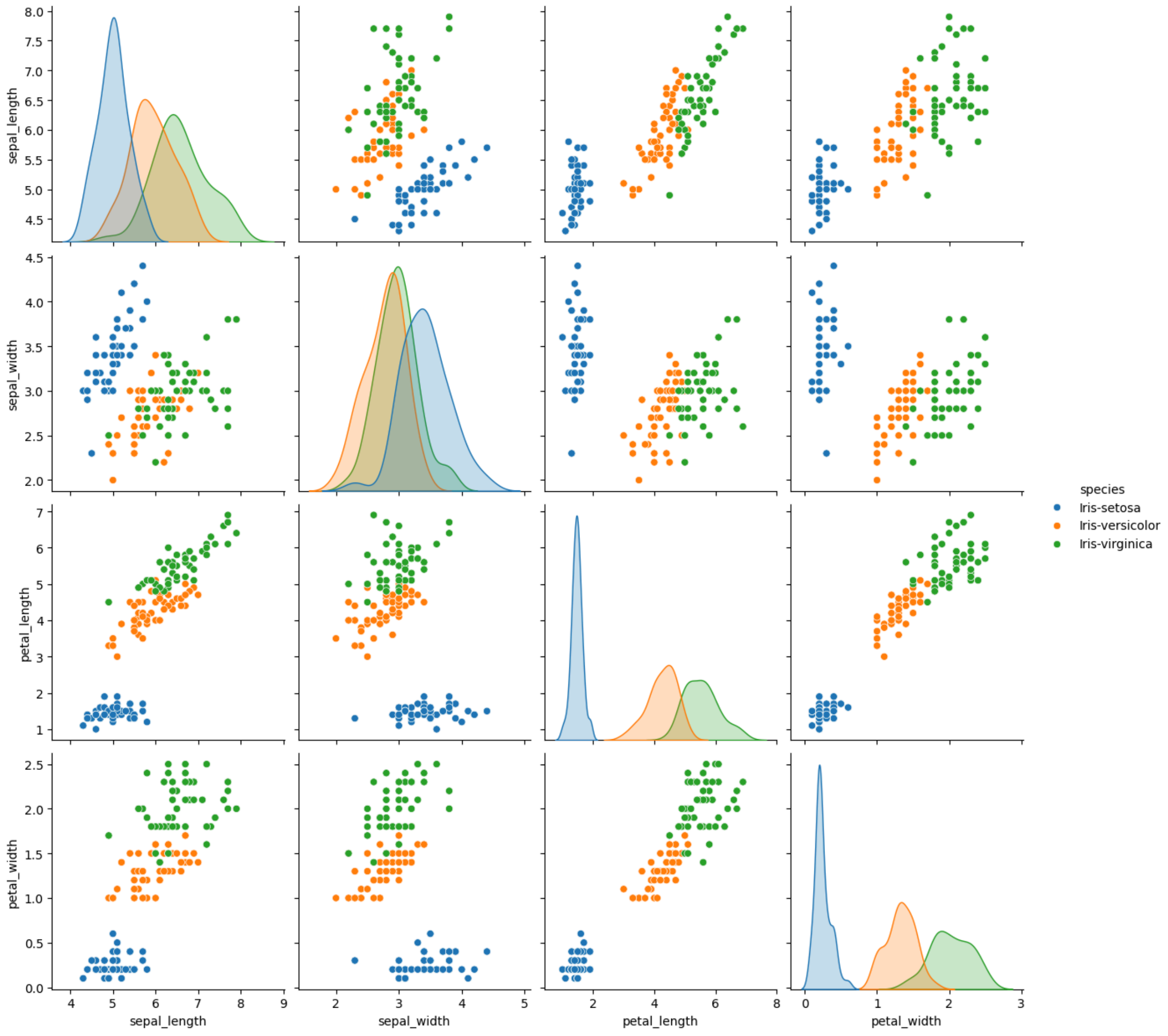
Pairplot for Feature Visualization

In this code, we create a **pairplot** using Seaborn to visualize the relationships between all pairs of features in the dataset. The `hue` parameter is set to 'species', which means that different species will be represented by different colors in the plots. Each subplot displays a scatter plot for each pair of features along with the corresponding diagonal plots, which represent the distribution of individual features. This visualization helps in understanding the correlations between features and how they vary across different species.

```
In [51]: sns.pairplot(data=df , hue= 'species' , size=3)
```

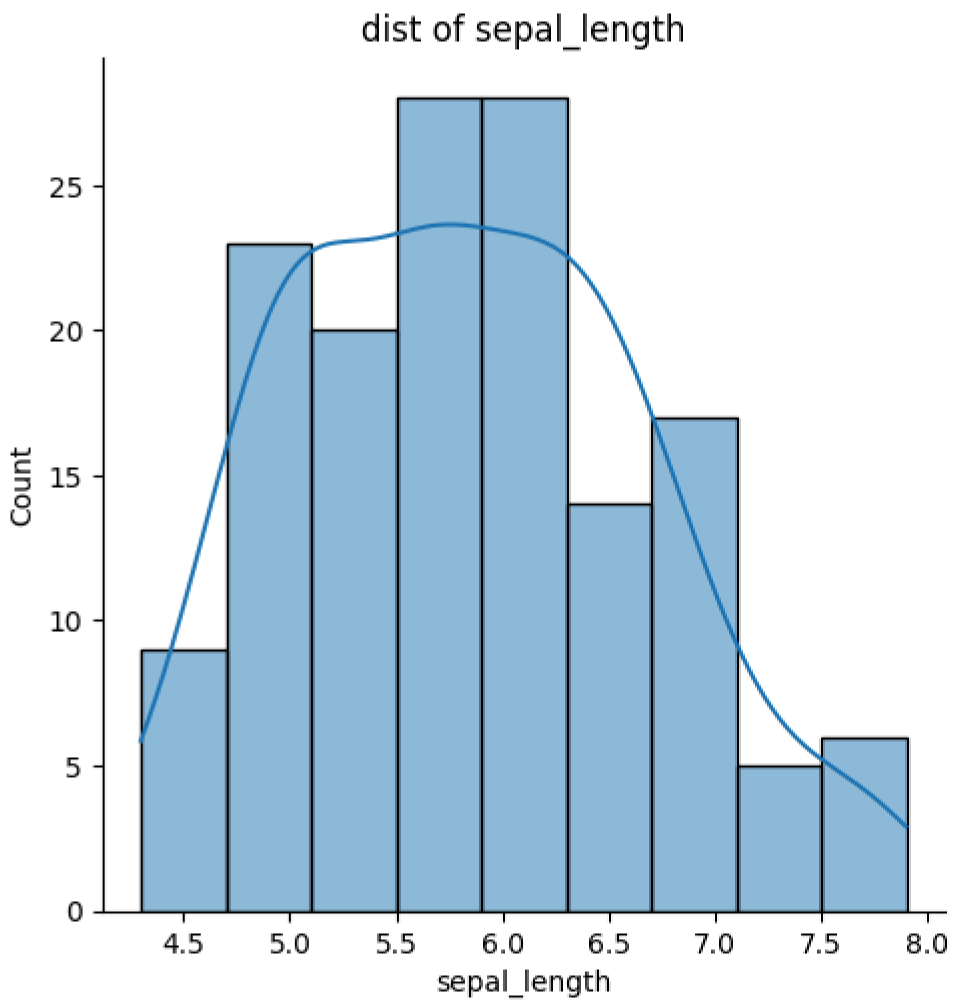
```
c:\Users\Mamzi\AppData\Local\Programs\Python\Python311\Lib\site-packages\seaborn\axi
sgrid.py:2100: UserWarning: The `size` parameter has been renamed to `height`; pleas
e update your code.
  warnings.warn(msg, UserWarning)
```

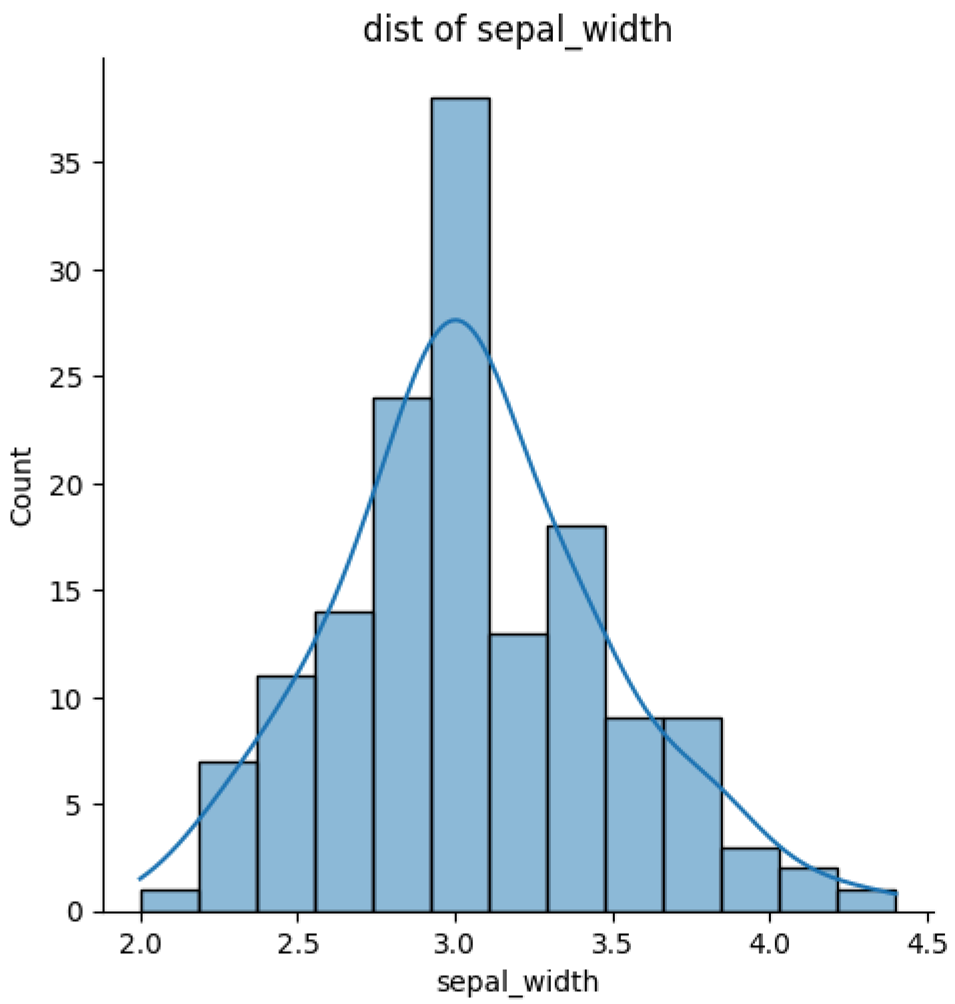
```
Out[51]: <seaborn.axisgrid.PairGrid at 0x167e07aa890>
```

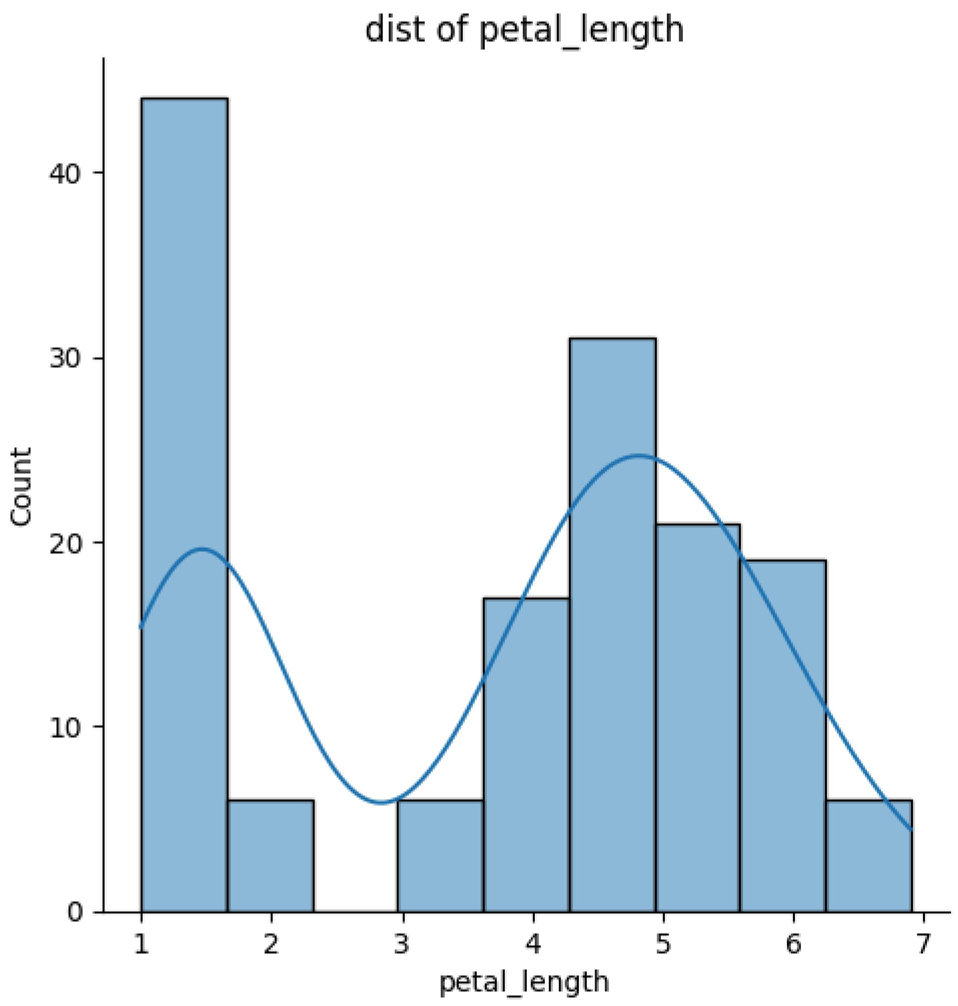


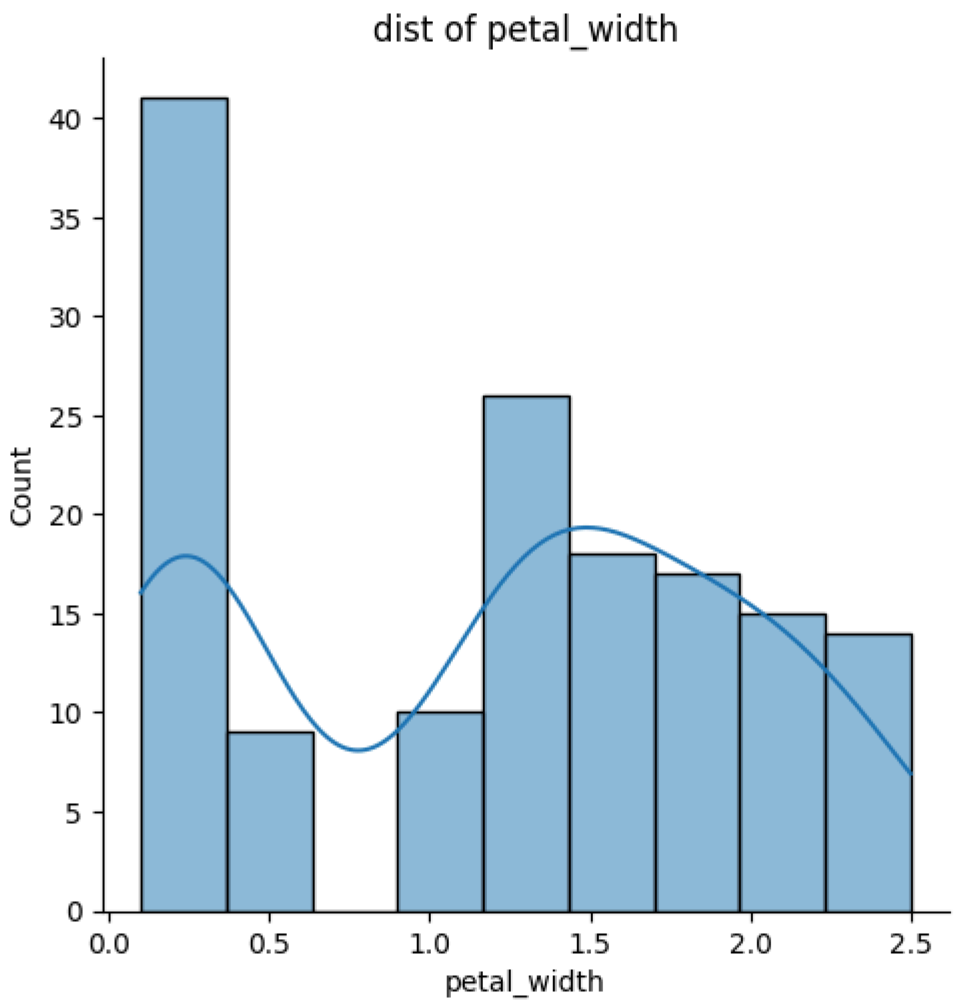
Distribution Plot for Features

In [52]:
```
for  feature in (features) :
    sns.displot(data= df ,x = feature , kde = True)
    plt.title(f'dist of {feature}')
    plt.show()
```


dist of sepal_length
Count
25
20
15
10
5
0
4.5
5.0
5.5
6.0
6.5
7.0
7.5
8.0
sepal_length


dist of sepal_width
Count
sepal_width
0
5
10
15
20
25
30
35
2.0
2.5
3.0
3.5
4.0
4.5


dist of petal_length
Count
0
10
20
30
40
1
2
3
4
5
6
7
petal_length

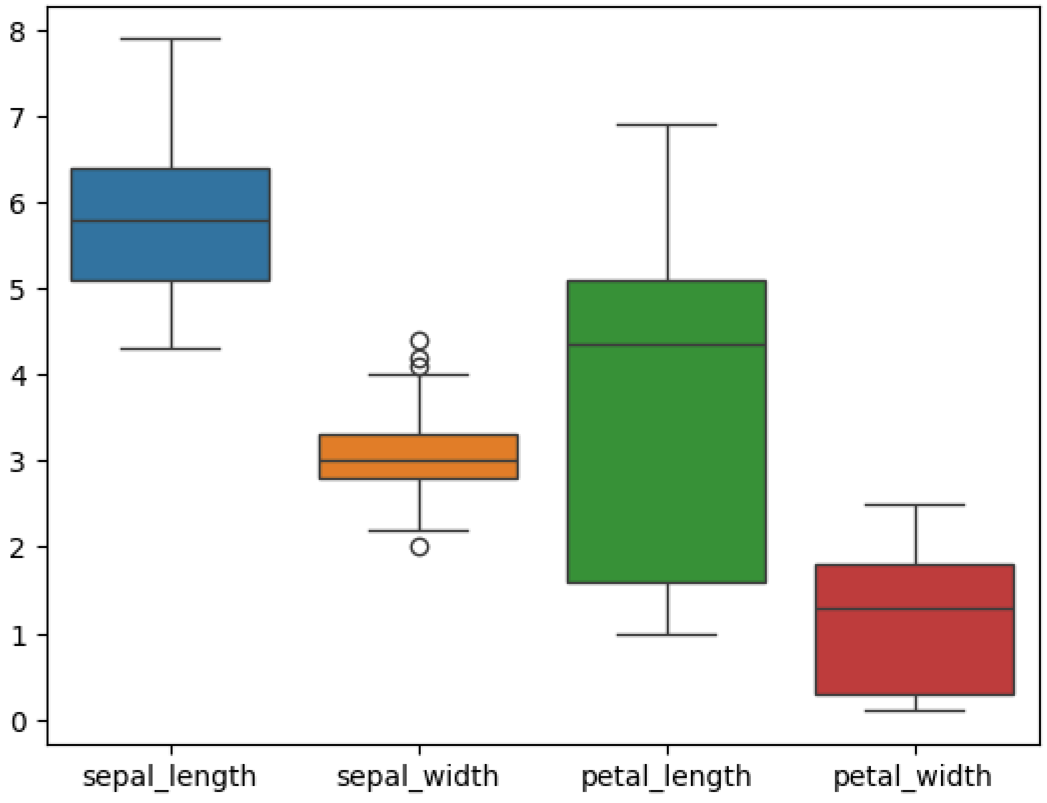


Boxplot and Outlier Handling

In this code, we first create a **boxplot** of the dataset to visualize the distribution of the features. We then calculate the **Interquartile Range (IQR)** for the 'sepal_width' feature, which is the difference between the 75th percentile (Q3) and the 25th percentile (Q1). Using the IQR, we define the minimum and maximum ranges for acceptable values. Any data points outside this range are considered **outliers**. We then replace the outliers in 'sepal_width' with the median of the feature to mitigate their effect. Finally, we create another boxplot to visualize the updated distribution after handling the outliers.

```
In [53]: sns.boxplot(data= df)
```

```
Out[53]: <Axes: >
```

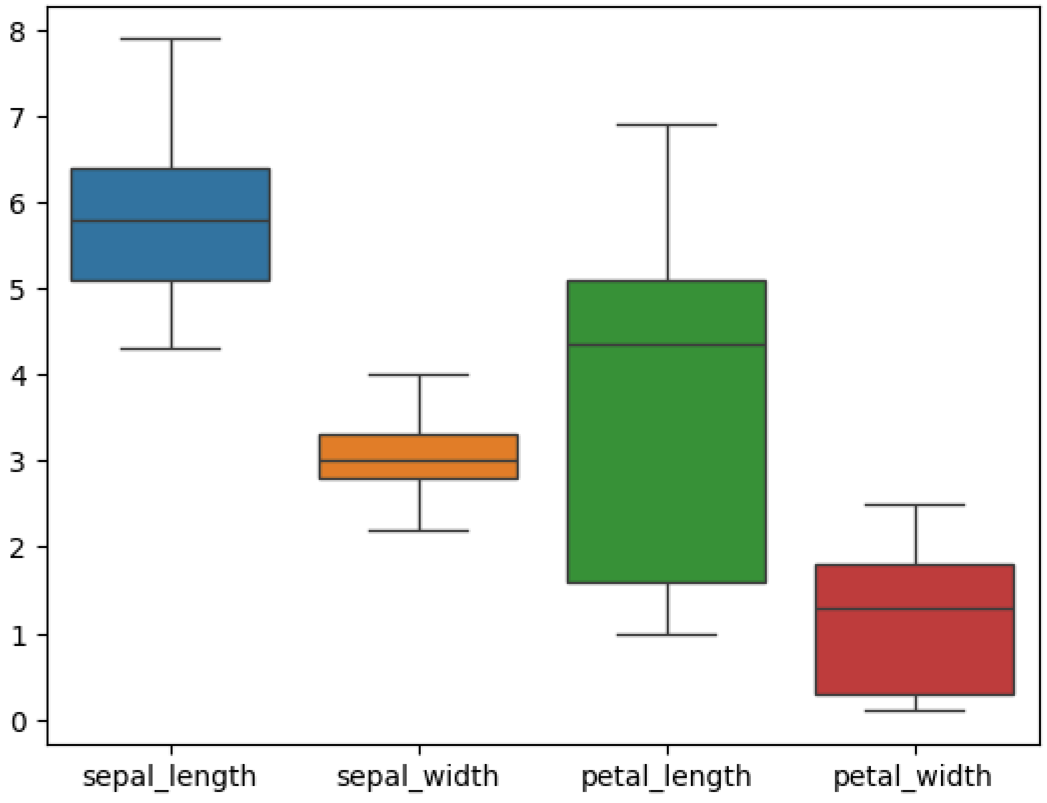


In [54]:
```
q1 = df['sepal_width'].quantile(0.25)
q3 = df['sepal_width'].quantile(0.75)
IQR = q3 - q1
min_range = q1 - 1.5 * IQR
max_range = q3 + 1.5 * IQR

outliers_mask = (df['sepal_width'] < min_range) | (df['sepal_width'] > max_range)
df.loc[outliers_mask, 'sepal_width'] = int(np.median(df['sepal_width']))
```

In [55]:
```
sns.boxplot(data= df)
```

Out[55]:
```
<Axes: >
```



K-Means Clustering

In this code, we are applying the **K-Means clustering algorithm** to the dataset to find the optimal number of clusters. The algorithm runs for different values of K (from 1 to 10) and calculates the **inertia** (Within-Cluster Sum of Squares, WCSS) for each value of K. The inertia represents how tightly the data points are grouped around the centroids, and we aim to minimize this value. The results can be used in the **Elbow Method** to determine the optimal number of clusters.

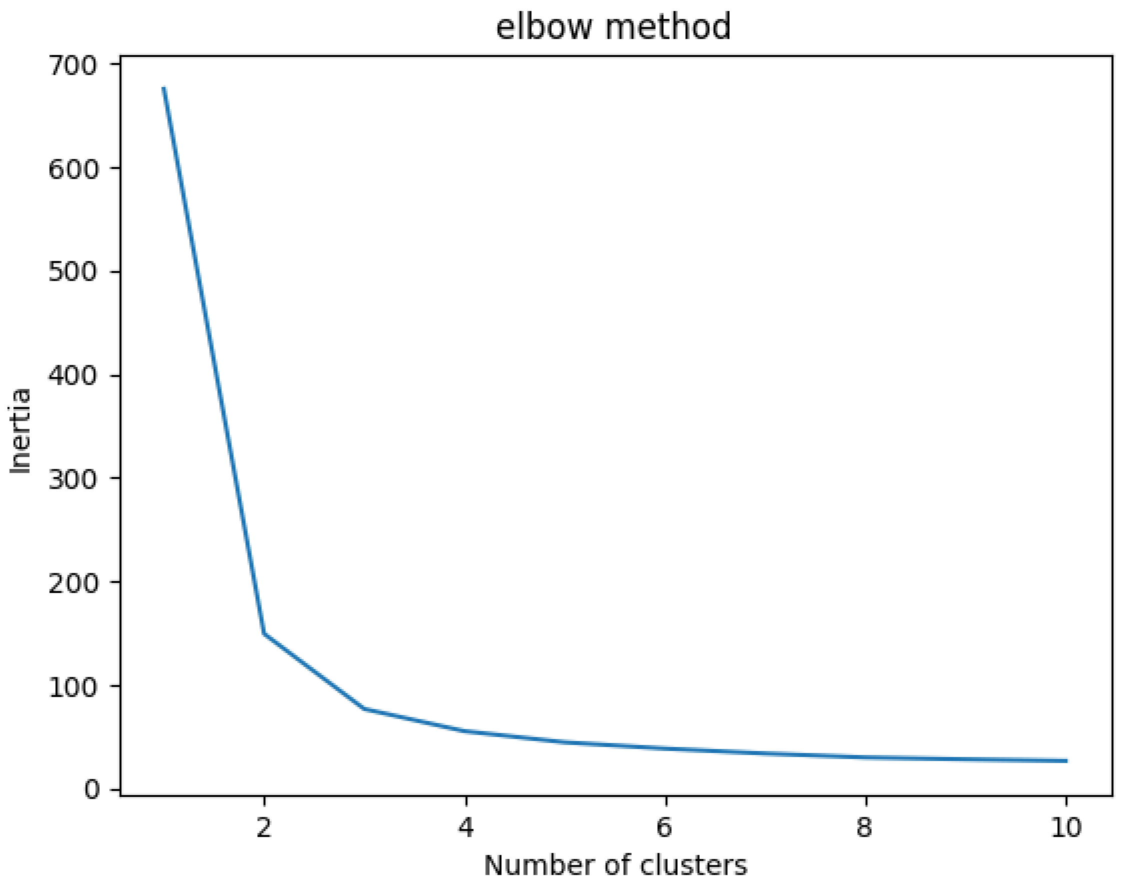
In [56]:
```
from sklearn.cluster import KMeans
inertia = []
x = df.drop('species' , axis= 1)

for i in range(1, 11):
    kmeans = KMeans(n_clusters = i , max_iter = 500, n_init = 10, random_state = 42
    kmeans.fit(x)
    inertia.append(kmeans.inertia_)
```

Elbow Method

The *Elbow Method* is a technique used to determine the **optimal number of clusters (K)** in K-Means clustering. It works by plotting the **Within-Cluster Sum of Squares (WCSS)** against the number of clusters. As the number of clusters increases, WCSS decreases, but the rate of decrease slows down. The "elbow" point, where the decrease becomes less significant, indicates the **optimal number of clusters**.

In [57]:
```
plt.plot(range(1, 11), inertia)
plt.title('elbow method')
plt.xlabel('Number of clusters')
plt.ylabel('Inertia')
plt.show()
```



In this analysis, the plot shows a noticeable "elbow" at K=3, suggesting that this is the optimal number of clusters to consider. At this point, adding more clusters yields diminishing returns in terms of reducing inertia, indicating that the data can be effectively partitioned into 3 distinct clusters.

In [58]:
```
model = KMeans(n_clusters = 3 , max_iter = 500, n_init = 10, random_state = 42)
y = model.fit_predict(x)
```

In [59]:
```
print(y)
```

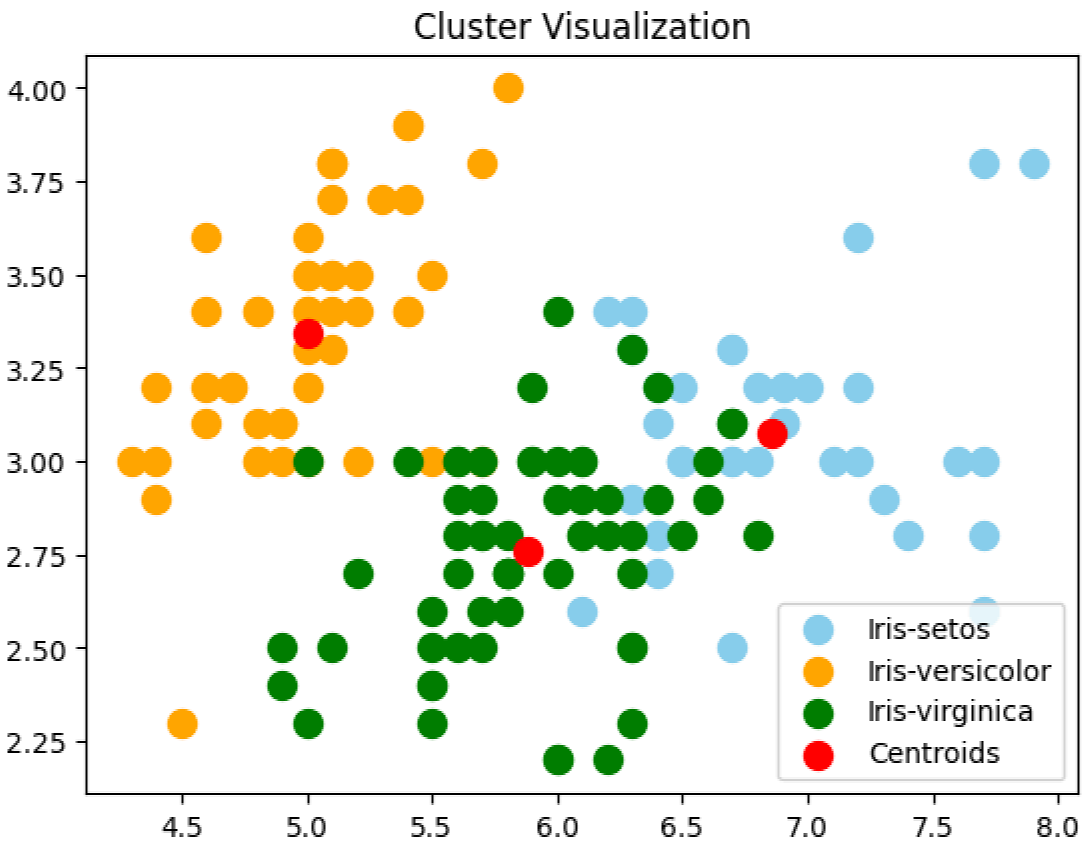
```
[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
 1 1 1 1 1 1 1 1 1 1 1 1 1 0 2 0 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
 2 2 2 0 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 0 2 0 0 0 0 2 0 0 0 0
 0 0 2 2 0 0 0 0 2 0 2 0 2 0 0 2 2 0 0 0 0 0 2 0 0 0 0 2 0 0 0 2 0 0 0 2 0
 0 2]
```

In [60]:
```
model.cluster_centers_
```

Out[60]:
```
array([[6.85384615, 3.07692308, 5.71538462, 2.05384615],
       [5.006     , 3.344     , 1.464     , 0.244     ],
       [5.88360656, 2.75737705, 4.38852459, 1.43442623]])
```

In [61]:
```
x = np.array(x)
y = np.array(y)
plt.scatter(x[y == 0, 0], x[y == 0, 1], s=100, c='skyblue', label='Iris-setos')
plt.scatter(x[y == 1, 0], x[y == 1, 1], s=100, c='orange', label='Iris-versicolor')
plt.scatter(x[y == 2, 0], x[y == 2, 1], s=100, c='green', label='Iris-virginica')

plt.scatter(model.cluster_centers_[:, 0], model.cluster_centers_[:, 1], s=100, c='r
plt.title('Cluster Visualization')
plt.legend()
plt.show()
```



Silhouette_score

In [62]:
```
silhouette_score(x , y)
```

Out[62]:
```
0.5531602359821158
```